IN THE SPECIFICATION:

Please amend Table 1 on page 32 as follows:

Table 1. Mesothelin peptides predicted to bind to HLA A2, A3, and A24.

HLA-Restriction	Amino Acid Sequence		Amino Acid Position in Protein
HLA-A2	SLLFLLFSL	(SEQ ID NO:1)	Mesothelin $A2_{(20-28)}$
HLA-A2	VLPLTVAEV	(SEQ ID NO:2)	Mesothelin $A2_{(530-538)}$
HLA-A2	LLALLMAGL	(SEQ ID NO:13)	PSCA $A2_{(5-13)}$
HLA-A2	ALQPGTALL	(SEQ ID NO:14)	PSCA $A2_{(14-22)}$
HLA-A2	ALLPALGLL	(SEQ ID NO:15)	PSCA $A2_{(108-116)}$
HLA-A3	ELAVALAQK	(SEQ ID NO:3)	Mesothelin $A3_{(83-92)}$
HLA-A3	ALQGGGPPY	(SEQ ID NO:4)	Mesothelin $A3_{(225-234)}$
HLA-A3	ALQPAAAIL	(SEQ ID NO:16)	PSCA $A3_{(99-107)}$
HLA-A3	LLALLMAGL	(SEQ ID NO:13)	PSCA $A3_{(5-13)}$
HLA-A3	ALQPGTALL	(SEQ ID NO:14)	PSCA $A3_{(14-22)}$
HLA-A3	LLPALGLLL	(SEQ ID NO:17)	PSCA $A3_{(109-117)}$
HLA-A3	QLGEQCWTA	(SEQ ID NO:18)	PSCA $A3_{(43-51)}$
HLA-A3	ALLCYSCKA	(SEQ ID NO:19)	PSCA $A3_{(20-28)}$
HLA-A24	FYPGYLCSL	(SEQ ID NO:5)	Mesothelin $A24_{(435-444)}$
HLA-A24	LYPKARLAF	(SEQ ID NO:6)	Mesothelin $A24_{(475-484)}$
HLA-A24	DYYVGKKNI	(SEQ ID NO:20)	PSCA $A24_{(76-84)}$
HLA-A24	ALLPALGLL	(SEQ ID NO:15)	PSCA $A24_{(108-116)}$
HLA-A24	ALQPAAAIL	(SEQ ID NO:16)	PSCA $A24_{(99-107)}$
HLA-A24	LLPALGLLL	(SEQ ID NO:17)	PSCA $A24_{(109-117)}$
HLA-A24	YYVGKKNIT	(SEQ ID NO:21)	PSCA $A24_{(77-85)}$

The three peptides, HIV-gag $A2_{77-85}$ (SLYNTVATL) (SEQ ID NO:7) (48), HIV-NEF $A3_{94-103}$ (QVPLRPMTYK) (SEQ ID NO:8) (49), and tyrosinase $A24_{206-214}$ (AFLPWHRLF) (SEQ ID NO:9) (50), are previously published epitopes that were used as control peptides for HLA-A2, A3, and A24 binding, respectively. The Mesothelin $A1_{309-318}$ binding epitope (EIDESLIFY) (SEQ ID NO:22) was used as a negative control peptide for all binding studies. The M1 peptide $(GILGFVFTL)_{58-66}$ (SEQ ID NO:10) (Gotch et al 1988) was used as a positive control for all of the HLA-A2 studies.

Please amend paragraph [29] on page 10 as follows:

Fig. 10 shows expression of murine mesothelin in WF-3 tumor cells demonstrated by RT-PCR with gel electrophoresis. Fig. 10. RT-PCR. RT-PCR was performed using the Superscript One-Step.RT-PCR Kit (Gibco, BRL) and a set of primers: ~~5'-CCCGAATTCATGGCCTTGCCAACAGCTCGA-3'~~ 5'-CCCGAATTCATGGCCTTGCCAACAGCTCGA-3' (SEQ ID NO: 11) and ~~5'-TATGAATCCGCTCAGCCTTAAAGCTGGGAG-3'~~ 5'-TATGGAATCCGCTCAGCCTTAAAGCTGGGAG-3' (SEQ ID NO: 12). Lane 1, size marker. Lane 2, RNA from W-3 cells and Lane 3, RNA from mesothelin-negative B 16 tumor cells. Specific amplification (indicated by an arrow) was observed in Lane 2 (WF-3 cells) but not in the Lane 3 (B16 cells).

Please amend paragraph [23], which starts on page 7, as follows:

Fig. 4A to 4D shows an ELISPOT analysis of CD8+ T-cells from PBMCs. No post-vaccination induction was observed of PSCA-specific T-cells in DTH responders or non-DTH responders who received an allogeneic GM-CSF-secreting tumor vaccine for pancreatic cancer. Fig. 4A. ELISPOT analysis of PBL from two patients who were HLA-A3 positive; Fig. 4B. ELISPOT analysis of PBL from two patients who were HLA-A 2 and HLA-A3 positive; Fig. 4C. ELISPOT analysis of PBL from two patients who were HLA-A24 positive. Fig. 4D. ELISPOT analysis of PBL from eight patients who were non-responders. ELISPOT analysis for IFN-γ-expressing cells was performed using PBMC that were isolated on the day prior to vaccination or 28 days following each of the vaccination. Lymphocytes were isolated by ficoll-hypaque separation and stored frozen in liquid nitrogen until the day of assay. CD8+ T-cell enrichment was performed prior to analysis. T2-A3 cells were pulsed with the six PSCA derived epitopes: PSCAA3(7-15) (closed squares), PSCAA3(52-60) (closed diamond), PSCAA3(109-117) (SEQ ID: 17) (closed triangle), PSCAA3(43-51) (SEQ ID: 18) (open square), PSCAA3(20-28) (SEQ ID: 19) (open diamond), and PSCAA3(99-107) (SEQ ID: 16) (open triangle). Negative HIV-NEFA3 (94-103) values were subtracted out. T2-A2 cells were pulsed with the three PSCA derived epitopes: PSCAA2(5-13) (SEQ ID: 13) (closed squares), PSCAA2(14-22)

(SEQ ID: 14) (closed diamonds), PSCAA2(108-116) (SEQ ID: 15) (closed triangles). Negative HIV-GAG(77-85) values were subtracted out. T2-A24 cells were pulsed with the five PSCA derived epitopes: PSCAA24(76-84) (SEQ ID: 20) (closed diamond), PSCAA24(77-85) (SEQ ID: 21) (star), PSCAA24(109-117) (SEQ ID: 17) (closed triangles), PSCAA24(108-116) (SEQ ID: 15) (closed circle), and PSCAA24(99-107) (SEQ ID: 16) (open triangle). Negative Tyrosinase A24(206-214) (SEQ ID: 9) values were subtracted. All DTH responders are represented by red lines, and DTH non-responders are represented by black lines. For the detection of nonspecific background, the number of IFN-γ spots for CD8+ T-cells specific for the irrelevant control peptides were counted. The HLA-A2 binding HIV-GAG protein derived epitope (SLYNTVATL; SEQ ID NO: 7), the HLA-A3 binding HIV-NEF protein derived epitope (QVPLRPMTYK; SEQ ID NO: 8), and the HLA-A24 binding tyrosinase protein derived epitope (AFLPWHRLF; SEQ ID NO: 9) were used as negative control peptides in these assays. Data represents the average of each condition assayed in triplicate and standard deviations were less than 5%. The number of human interferon gamma (hIFNg) spots per 105 CD8+ T-cells is plotted. Analysis of each patient's PBL was performed at least twice.

Please amend paragraph [132], which starts on page 56, as follows:

Fig. 10 shows expression of murine mesothelin in WF-3 tumor cells as demonstrated by RT-PCR with gel electrophoresis. Western blot analysis was also performed to confirm expression (not shown). As shown in Fig. 10, RT-PCR was performed using the Superscript One-Step RT-PCR Kit (Gibco, BRL) and a set of primers: ~~5'-CCCGAATTCATGGCCTTGCCAA-CAGCTCGA-3'~~ 5'-CCCGAATTCATGGCCTTGCCAACAGCTCGA-3' and 5'-TATGGATCCGCTCA GCCTTAAAGCTGGGAG-3' (SEQ ID NOS: 11 and 12, respectively). Western blot analysis was also used to demonstrate the expression of mesothelin protein in WF-3 tumor cells. Tumor cells were stained with anti-mesothelin mouse polyclonal antibody followed by FITC-conjugated goat anti-mouse IgG secondary antibody (data not shown).

Please substitute the enclosed sequence listing for the one currently part of the application.